



#4

SEQUENCE LISTING

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<120> Novel GPCR-Like Proteins and Nucleic Acids Encoding
Same

<130> 21402-224 AG

<140> 10/024444
<141> 2001-12-18

<150> 60/256635
<151> 2000-12-18

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<170> PatentIn Ver. 2.1

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<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Unknown

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atacatgttg gcaactgacca gcaatggtct gctgctcctg gccatcacca tagaagcccg 180
gctccacatg cccatgtacc tcctgcttgg gcagctctct ctcatggacc tcctgttcac 240
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tggaggctgt gcacttcaga tggtcctggc actgacaatg ggtagcgctg aggacctcct 360
actggccttc atggcctatg acaggtatgt ggccatttgt catcctctga aatacatgac 420
cctcatgagc ccaagagtct gctggatcat ggtggccaca tcctggatcc tggcatccct 480
gattgtctata ggacatacca tgtacactat gcacctccct ttctgtgtgt cctgggaaat 540
caggcatctg ctctgtgaga tcccaccctt gctgaagttg gcctgtgctg atacctccag 600
tgtagagctt ataataacg tgacaggtgt gactttcctc ttgctcccca tttctgcat 660
tgtggcctcc tacacactag tcctattcac tgtgcttcgt atgccatcaa atgaggggag 720
gaagaaagcc cttgtcacct gctcttccca cctgattgtg gtcgggatgt tctatggagc 780
tgccacattc atgtatgtct tgcccagttc cttccacagc cccaaacaag acaacatcat 840
ctctgttttc tacacaattg tcactccagc cctgaatcca ctcatctaca gcctgaggaa 900
taaggaggct atgcgggcct tgaggagggt cctgggaaaa tacatactgc tggcacattc 960
cacgctctag ggaagga 977

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 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

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 Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
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 Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
 35 40 45
 Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
 50 55 60
 Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
 130 135 140
 Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
 145 150 155 160
 Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
 195 200 205
 Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
 210 215 220
 Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr

	245		250		255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn					
	260		265		270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu					
	275		280		285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val					
	290		295		300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu					
	305		310		315

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20 25 30
Ile Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Ala
35 40 45
Ile Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
50 55 60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
65 70 75 80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
85 90 95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp
100 105 110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115 120 125
Pro Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met
130 135 140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr
145 150 155 160
Val Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His
165 170 175
Leu Leu Cys Glu Ile Pro His Leu Leu Lys Val Ala Cys Ala Asp Thr
180 185 190

Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
 195 200 205

Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr
 210 215 220

Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240

Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270

Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300

Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 305 310 315

<210> 4

<211> 316

<212> PRT

<213> mouse

<400> 4

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Ile Leu Asn Gly Ser Ser Ser Pro Glu Leu Leu Cys Ala Ile Val Thr
 20 25 30

Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val
 35 40 45

Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60

Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80

Ala Val Met Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Gly Gly
 85 90 95

Cys Ala Leu Gln Met Ala Leu Ala Leu Met Leu Gly Ser Ala Glu Asp
 100 105 110

Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125

Pro Leu Asn Tyr Met Val Phe Met Ser Pro Thr Val Cys Trp Leu Ile
 130 135 140

Val Ser Thr Ser Trp Ile Leu Ala Ser Leu Thr Ala Val Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Leu Pro Leu Leu Lys Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Thr Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Val Thr Ser Tyr Thr Leu Ile Leu Ser Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Lys Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Leu Ser His Leu Met Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Leu His Ser Ala Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Leu Arg Arg Val
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 Leu Gly Arg Tyr Ile Leu Pro Ala His Leu Thr Leu
 305 310 315

<210> 5
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 <212> PRT
 <213> mouse

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 Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr
 20 25 30
 Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly

85										90					95				
Cys	Ala	Leu	Gln	Leu	Phe	Ser	Ala	Met	Thr	Leu	Gly	Gly	Ala	Glu	Asp				
			100					105						110					
Leu	Leu	Leu	Ala	Phe	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His				
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Pro	Leu	Asn	Tyr	Met	Ile	Phe	Met	Ser	Pro	Lys	Ala	Cys	Arg	Leu	Met				
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Val	Ala	Ile	Ser	Trp	Ile	Leu	Ala	Ser	Leu	Ser	Ala	Leu	Gly	His	Thr				
	145				150					155					160				
Val	Tyr	Thr	Met	His	Phe	Pro	Phe	Cys	Met	Ser	Gln	Glu	Ile	Arg	His				
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Leu	Leu	Cys	Glu	Val	Pro	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr				
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Ser	Gln	Tyr	Glu	Leu	Met	Val	Tyr	Val	Thr	Gly	Val	Ile	Phe	Leu	Leu				
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Leu	Pro	Leu	Ser	Ala	Ile	Ile	Thr	Ser	Tyr	Ser	Leu	Ile	Leu	Phe	Thr				
	210					215					220								
Val	Leu	His	Met	Pro	Ser	Asn	Glu	Gly	Arg	Lys	Lys	Ala	Leu	Val	Thr				
	225				230					235					240				
Cys	Ser	Ser	His	Leu	Thr	Val	Val	Gly	Met	Phe	Tyr	Gly	Gly	Ala	Thr				
			245						250					255					
Phe	Met	Tyr	Val	Leu	Pro	Ser	Ser	Phe	His	Ser	Pro	Lys	Gln	Asp	Asn				
			260					265					270						
Ile	Ile	Ser	Val	Phe	Tyr	Thr	Ile	Val	Thr	Pro	Ala	Leu	Asn	Pro	Leu				
		275					280					285							
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 <212> PRT
 <213> mouse

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Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr
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Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Glu
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met
 130 135 140
 Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val
 290 295 300
 Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val
 305 310 315

<210> 7
 <211> 316

<212> PRT
<213> mouse

<400> 7

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		20						25					30			
Ala	Leu	Tyr	Met	Leu	Ala	Leu	Ile	Ser	Asn	Gly	Leu	Leu	Ile	Leu	Val	
		35					40					45				
Ile	Thr	Met	Asp	Ala	Arg	Leu	His	Val	Pro	Met	Tyr	Phe	Leu	Leu	Gly	
	50					55					60					
Gln	Leu	Ser	Leu	Met	Asp	Leu	Leu	Phe	Thr	Ser	Val	Val	Thr	Pro	Lys	
65					70					75					80	
Ala	Val	Ile	Asp	Phe	Leu	Leu	Arg	Asp	Asn	Thr	Ile	Ser	Phe	Glu	Gly	
				85					90					95		
Cys	Ser	Leu	Gln	Met	Phe	Leu	Ala	Leu	Thr	Leu	Gly	Gly	Ala	Glu	Asp	
			100					105					110			
Leu	Leu	Leu	Ala	Phe	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	
		115					120					125				
Pro	Leu	Asn	Tyr	Met	Ile	Phe	Met	Arg	Pro	Ser	Ile	Cys	Trp	Leu	Met	
	130					135					140					
Val	Ala	Thr	Ser	Trp	Val	Leu	Ala	Ser	Leu	Met	Ala	Leu	Gly	Tyr	Thr	
145					150					155					160	
Thr	Tyr	Thr	Met	Gln	Tyr	Ser	Tyr	Cys	Lys	Ser	Arg	Lys	Ile	Arg	His	
				165					170					175		
Leu	Leu	Cys	Glu	Ile	Pro	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	
			180					185					190			
Ser	Lys	Tyr	Glu	Leu	Met	Val	Tyr	Val	Met	Gly	Val	Thr	Phe	Leu	Ile	
		195					200					205				
Pro	Pro	Leu	Ala	Ala	Ile	Leu	Ala	Ser	Tyr	Ser	Leu	Ile	Leu	Phe	Thr	
	210					215					220					
Val	Leu	His	Met	Pro	Ser	Asn	Glu	Gly	Arg	Lys	Lys	Ala	Leu	Val	Thr	
225					230					235					240	
Cys	Ser	Ser	His	Leu	Thr	Val	Val	Gly	Met	Phe	Tyr	Gly	Ala	Ala	Thr	
				245					250					255		
Phe	Met	Tyr	Val	Leu	Pro	Asn	Ser	Phe	His	Ser	Pro	Arg	Gln	Asp	Asn	
			260					265					270			
Ile	Ile	Ser	Val	Phe	Tyr	Thr	Ile	Val	Thr	Pro	Ala	Leu	Asn	Pro	Leu	
			275				280					285				

Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Leu Ile Arg Val
290 295 300

Leu Gly Arg Tyr Ile Val Pro Ala His Pro Thr Leu
305 310 315

<210> 8
<211> 17
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Protein motif

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<221> VARIANT
<222> (1)
<223> X1 wherein X aa is G, or S, or T, or A, or L, or
I, or V, or M, or F, or Y, or W, or C

<220>
<221> VARIANT
<222> (2)
<223> X2 wherein X aa is G, or S, or T, or A, or N, or
C, or C, or P, or D, or E

<220>
<221> VARIANT
<222> (3)
<223> X3 wherein X aa is E, or D, or P, or K, or R, or H

<220>
<221> VARIANT
<222> (4)
<223> X4 wherein X aa is any amino acid

<220>
<221> VARIANT
<222> (5)
<223> X5 wherein X aa is any amino acid

<220>
<221> VARIANT
<222> (6)
<223> X6 wherein X aa is L, or I, or V, or M, or N, or
Q, or G, or A

<220>
<221> VARIANT
<222> (7)
<223> X7 wherein X aa is any amino acid

<220>
<221> VARIANT
<222> (8)

<223> X8 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (9)

<223> X9 wherein X aa is L, or I, or V, or M, or F, or T

<220>

<221> VARIANT

<222> (10)

<223> X10 wherein X aa is G, or S, or T, or A, or N, or
C

<220>

<221> VARIANT

<222> (11)

<223> X11 where X aa is L, or I, or V, or M, or F, or Y,
or W, or S, or T, or A, or C

<220>

<221> VARIANT

<222> (12)

<223> X12 wherein X aa is D, or E, or N, or H

<220>

<221> VARIANT

<222> (13)

<223> X13 wherein X aa is F, or Y, or, W, or W, or C, or
S, or H

<220>

<221> VARIANT

<222> (14)

<223> X14 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (15)

<223> X15 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (16)

<223> X16 wherein X aa is l, or I, or V, or M

<400> 8

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 9

<211> 254

<212> PRT

<213> Unknown Organism

<400> 9

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
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Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe
50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile
65 70 75 80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg
85 90 95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser
130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Val Leu
145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu
165 170 175

Arg Lys Arg Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr
245 250

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

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tgccacattc atgtatgtct tg

22

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 11

cacagcccca aacaagacaa catcat

26

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 12

ggctggagtg acaatttgtg ag

22